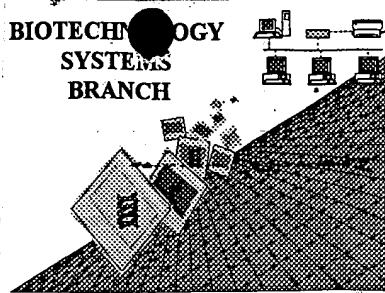


Sanaya

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED

NOV 28 2000

#17
TECH 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/306,333

Source: 1655

Date Processed by STIC: 11/16/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/306,333

DATE: 11/25/2000
TIME: 01:06:57

INPUT SET: S3614340

RECEIVED

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

NOV 28 2000

TECH CENTER 1600/2900

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

1
2
3 (1) General Information:
4 (i) APPLICANT: Vijg, Jan
5 (ii) TITLE OF INVENTION: BRCA1 And hMLH1 Gene Primer Sequences And
6 Method For Testing
7 (iii) NUMBER OF SEQUENCES: 122
8 (iv) CORRESPONDENCE ADDRESS:
9 (A) ADDRESSEE: Rines & Rines
10 (B) STREET: 81 North State Street
11 (C) CITY: Concord
12 (D) STATE: NH
13 (E) COUNTRY: USA
14 (F) ZIP: 03301
15 (v) COMPUTER READABLE FORM:
16 (A) MEDIUM TYPE: Diskette, 3.50 inch
17 (B) COMPUTER: IBM PC
18 (C) OPERATING SYSTEM: MS-DOS
19 (D) SOFTWARE: Microsoft Wordpad
20 (vi) CURRENT APPLICATION DATA:
21 (A) APPLICATION NUMBER: US/09/306,333
22 (B) FILING DATE: 06-May-1999
23 (C) CLASSIFICATION: <Unknown>
24 ((vii) PRIOR APPLICATION DATA) → delete, if no information
25 (viii) ATTORNEY/AGENT INFORMATION: given
26 (A) NAME: Rines, Robert H.
27 (B) REGISTRATION NUMBER: 15,932
28 (ix) TELECOMMUNICATION INFORMATION:
29 (A) TELEPHONE: (603) 228-0121
30 (B) TELEFAX: (603) 228-0210

ERRORED SEQUENCES FOLLOW:

355 (2) INFORMATION FOR SEQ ID NO:19:
356 (i) SEQUENCE CHARACTERISTICS:
357 (A) LENGTH: 20 base pairs
358 (B) TYPE: nucleic acid
359 (C) STRANDEDNESS: double stranded
360 (D) TOPOLOGY: linear
361 (ii) MOLECULE TYPE: genomic DNA
362 (iii) HYPOTHETICAL: no
363 (iv) ANTI-SENSE: no

next page

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/306,333DATE: 11/25/2000
TIME: 01:06:57

INPUT SET: S36143.raw

364 (vi) ORIGINAL SOURCE:
365 (A) ORGANISM: human
366 (vii) IMMEDIATE SOURCE:
367 (A) LIBRARY: genomic
368 (viii) POSITION IN GENOME:
369 (A) CHROMOSOME/SEGMENT: 3
370 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
--> 371 CTTGCTCCTT CATGTTCTTG
372

18 20

605 (2) INFORMATION FOR SEQ ID NO:34:
606 (i) SEQUENCE CHARACTERISTICS:
--> 607 (A) LENGTH: 18 base pairs 37 shown
608 (B) TYPE: nucleic acid
609 (C) STRANDEDNESS: double stranded
610 (D) TOPOLOGY: linear
611 (ii) MOLECULE TYPE: genomic DNA
612 (iii) HYPOTHETICAL: no
613 (iv) ANTI-SENSE: no
614 (vi) ORIGINAL SOURCE:
615 (A) ORGANISM: human
616 (vii) IMMEDIATE SOURCE:
617 (A) LIBRARY: genomic
618 (viii) POSITION IN GENOME:
619 (A) CHROMOSOME/SEGMENT: 17
620 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
621 GAGAAAGAAT GAATTGGAGT TGGATTTTCG TTCTCAC
622

37

2027 (2) INFORMATION FOR SEQ ID NO:113:
2028 (i) SEQUENCE CHARACTERISTICS:
--> 2029 (A) LENGTH: 19 base pairs 18 shown
2030 (B) TYPE: nucleic acid
2031 (C) STRANDEDNESS: double stranded
2032 (D) TOPOLOGY: linear
2033 (ii) MOLECULE TYPE: genomic DNA
2034 (iii) HYPOTHETICAL: no
2035 (iv) ANTI-SENSE: no
2036 (vi) ORIGINAL SOURCE:
2037 (A) ORGANISM: human
2038 (vii) IMMEDIATE SOURCE:
2039 (A) LIBRARY: genomic
2040 (viii) POSITION IN GENOME:
2041 (A) CHROMOSOME/SEGMENT: 17
2042 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
--> 2043 ATTCCCCTGT CCCTCTCT
2044

18 19

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/306,333DATE: 11/25/2000
TIME: 01:06:58**INPUT SET: S36143.raw**

Line	Error	Original Text
23	Wrong Classification	(C) CLASSIFICATION: <Unknown>
371	# of Sequences for line conflicts w/ running total	CTTGCTCCTT CATGTTCTTG
607	Entered (18) and Calc. Seq. Length (37) differ	(A) LENGTH: 18 base pairs
2029	Entered (19) and Calc. Seq. Length (18) differ	(A) LENGTH: 19 base pairs
2043	# of Sequences for line conflicts w/ running total	ATTCCCCTGT CCCTCTCT